Remarks

Amendments to the Claims

Each of independent claims 1, 12, 33, 52, and 59 is amended to recite that the biological subject is "obtained" from a region of the mammal. Similarly, each of independent claims 9, 22, and 62 is amended to recite that the second sample is "obtained" from the patient. The specification supports these amendments on page 22, line 11 to page 23, line 2, where it describes obtaining biological subjects and samples.

Each of independent claims 9, 22, and 62 is amended to clarify that the recited steps are carried out at two different time points during a therapeutic regimen. The specification supports this amendment on page 56, lines 13-23, which describes taking samples from patients "at various time points during the course of the application of a treatment regimen."

New claims 65 and 66 recite that the mammal or patient, respectively, is a human, and new claims 67-82 recite human hepsin sequences SEQ ID NO:1 (nucleotide) and SEQ ID NO:2 (amino acid), which are disclosed in the specification as filed.

The amendments do not add new matter

The Rejection of Claims 59-64 Under 35 U.S.C. § 112 ¶ 2

The Office Action maintains the rejection of claims 59-64 under 35 U.S.C. § 112 ¶ 2 because the recitations "first indirect measure" and "second indirect measure" allegedly are indefinite. Applicants respectfully traverse the rejection.

Under the second paragraph of 35 U.S.C. § 112, the relevant inquiry

... is merely to determine whether the claims do, in fact, set out and circumscribe a particular area with a reasonable degree of precision and particularity. It is here where the definiteness of the

language employed must be analyzed — not in a vacuum, but always in light of the teachings of the prior art and of the particular application disclosure as it would be interpreted by one possessing the ordinary level of skill in the pertinent art.

In re Moore, 439 F.2d 1232, 1235, 58 C.C.P.A. 1042, 1046-47 (1971) (footnote omitted). The Office Action contends that "[t]he terms, 'first indirect measure' or 'second indirect measure' are not defined by the claim(s), the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the metes and bounds of such terms." Office Action at page 3. On the contrary, one of ordinary skill in the art would understand that, in the context of determining gene copy number, any method other than directly counting copies of genes is, by definition, an indirect measure of gene copy number. Indirect methods of detecting gene copy number were well known in the art when this application was filed. As the specification teaches, these methods include Southern blotting, in situ hybridization, comparative genomic hybridization (CGH), amplification-based assays (e.g., a PCR-based TaqMan assay), and DNA microarray-based CGH (pages 41-43; Example 1). Each of these methods detects a measurement which reflects gene copy number and is, therefore, indirect. In the context of the specification and the knowledge of one of ordinary skill, the term "indirect measure" as used in claims 59-64 is definite.

Under 35 U.S.C. § 112, second paragraph, the claims must "reasonably apprise those skilled in the art both of the utilization and scope of the invention." Georgia-Pacific Corp. v. United States Plywood Corp., 258 F.2d 124, 136, 118 U.S.P.Q. 122, 130 (2d Cir. 1958), cert. denied, 358 U.S. 884 (1958). Claims 59-64 serve this purpose. Claims 59-64 are therefore definite.

Applicants respectfully request withdrawal of the rejection.

Rejection of Claims 1-3, 9-12, 22-24, 33-35, and 39-64 Under 35 U.S.C. § 112 ¶ 1

Claims 1-3, 9-12, 22-24, 33-35, and 39-64 stand rejected under 35 U.S.C. \S 112 \P 1 as insufficiently described. The Office Action asserts the term "hepsin" is broader than the description supports. Applicants respectfully traverse the rejection.

What is required to satisfy the written description requirement depends on the nature of the invention claimed. *In re DiLeone*, 436 F.2d 1404, 1405, 168 U.S.P.Q. 592, 593 (C.C.P.A. 1971). Independent claims 1, 52, and 59 recite a hepsin gene copy number in a biological subject obtained from a region of a mammal that is suspected to be precancerous or cancerous. Independent claims 9 and 62 recite a hepsin gene copy number in a sample of precancerous of cancer cells obtained from a patient. Independent claim 12 recites a test level of hepsin mRNA expression in a biological subject obtained from a region of the mammal that is suspected to be precancerous or cancerous. Independent claim 22 recites expression levels of at least one of hepsin mRNA or hepsin protein in samples of a biological subject comprising precancerous or cancer cells obtained from a patient. Independent claim 33 recites detecting a test hepsin protein expression level in a biological subject obtained from a region of the mammal that is suspected to be precancerous or cancerous. In each case, the recited hepsin gene, protein, or mRNA is one which naturally occurs in the mammal.

The naturally occurring mammalian hepsin protein and gene were well known in the art at the February 14, 2001 priority date of this application. See, e.g., Kawamura¹ and Vu² (mouse

¹ Kawamura et al., "Complete nucleotide sequence, origin of isoform and functional characterization of the mouse hepsin gene," Eur J Biochem, 1999 Jun;262(3):755-64.

² Vu et al., "Identification and Cloning of the Membrane-associated Scrine Protease, Hepsin, from Mouse Preimplantation Embryos," J. Biol. Chem. 272, 31315-20, 1997.

hepsin); Kazama³ and Leytus⁴ (human hepsin); and Farley (rat hepsin),⁵ each provided with the accompanying Information Disclosure Statement. An adequate written description of a gene which is well known in the art does not require a structural recitation either in the specification or in the claims. See Capon v. Eshhar, 418 F.3d 1349, 1360-61, 76 U.S.P.Q.2d 1078, 1087 (Fed. Cir. 2005) ("the Board erred in ruling that § 112 imposes a per se rule requiring recitation in the specification of the nucleotide sequence of claimed DNA, when that sequence is already known in the field."). Thus, the fact that the claims do not recite a sequence identifier "relating to hepsin" as noted in the Office Action at page 4 ¶ 1 does not mean that the claims lack written description. Under Capon, a sequence identifier is not required to describe the term "hepsin."

The Office Action cites nine different GenBank Accession Numbers as disclosing hepsin genes. Page $4 \ 1$. The hepsin coding sequences with these Accession Numbers, however, are not "highly variant," as the Office Action contends. *Id.*

Accession Numbers NM_017112 and X70900 are rat hepsin coding sequences; a BLAST alignment of these sequences shows that the two sequences are 100% identical (Exhibit 1). Accession Numbers NM_008281 and AF030065 are mouse hepsin coding sequences; a BLAST alignment of these sequences shows that the two sequences are 100% identical (Exhibit 2). The mouse and rat sequences are 94% identical (Exhibit 3).

Accession Numbers BC025716.1, NM_182983.1, NM_002151.1, X07732, and X07002.1 are human hepsin coding sequences. BLAST alignments of SEQ ID NO:1 with each of the other

³ Kazama et al., "Hepsin, a putative membrane-associated serine protease, activates human factor VII and initiates a pathway of blood coagulation on the cell surface leading to thrombin formation," J Biol Chem. 1995 Jan 6;270(1):66-72.

⁴ Leytus *et al.*, "A novel trypsin-like scrine protease (hepsin) with a putative transmembrane domain expressed by human liver and hepatoma cells," Biochemistry 27, 1067-1074, 1988.

⁵ Farley et al., "Cloning and sequence analysis of rat hepsin, a cell surface serine proteinase," Biochim Biophys Acta, 1993 Jun 25;1173(3):350-2.

human hepsin coding sequences are provided in Exhibits 4-8. SEQ ID NO:1 is 100% identical over 1593 contiguous nucleotides and 100% identical over 193 contiguous nucleotides with each of splice variants NM_182983.1 (Exhibit 5) and X07732 (Exhibit 7). SEQ ID NO:1 is 99% identical with BC025716.1 (Exhibit 4), 100% identical with NM_002151.1 (Exhibit 6), and 100% identical with 1199 contiguous nucleotides of X07002.1 (Exhibit 8). SEQ ID NO:1 is 83% identical to a long stretch (1318 nucleotides) of the rat and mouse hepsin coding sequences (Exhibit 9).

Mammalian hepsin coding sequences were known in the art when this application was filed, and none of the sequences cited in the Office Action are "highly variant." The specification therefore satisfies the written description requirement with respect to the term "hepsin" as recited in the rejected claims.

Applicants respectfully request withdrawal of the rejection.

Enablement Rejections

All of the pending claims stand rejected under 35 U.S.C. \S 112 \P 1 as not enabled for their full scope. In each case, the Office Action contends that the specification enables the claimed methods for *ex vivo* use but not for use *in vivo*. Office Action at page 7 \P 1. Applicants respectfully traverse the rejection.

To advance prosecution, each of the independent claims has been amended to clarify that the recited method steps are carried out ex vivo. Each of the independent diagnostic method claims (1, 12, 33, 52, and 59) now recites that the biological subject is "obtained from" a region of the mammal suspected to be precancerous or cancerous. Similarly, each of the independent methods of monitoring treatment efficacy (9, 22, and 62) recites that the sample is "obtained

from" a patient. Because the Office Action acknowledges this subject matter is enabled, Applicants respectfully request withdrawal of the rejection.

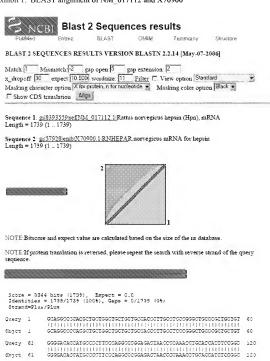
Respectfully submitted,
BANNER & WITCOFF, LTD.

/Lisa M. Hemmendinger/

By: Lisa M. Hemmendinger Registration No. 42,653

Customer No. 22907

Date: October 27, 2006



Query 121 GAACCCCAGGSTTCCGCCCCAGCCDAACAGGTCAACCTGGGAATCATTAACAAGAGTCCC 180

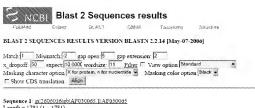
Shjet	223	${\tt GARCSOTASGGTTOSGGOCCAGGCCAACAGGTGAACCTGGGAATGATTAAGAAGAGTGCC}$	180
Onesa	191	TSACATOGCSAAGGAGGGTGOCCGGACTGCACCATGCTGTTCCAGACCCAAGGTGGGAGC	260
Shjet	181	TEACA TOGOGRAGGAGGGTGGCGGGRATTGCAGCTGTTTGCAGACGCAAGGTGGCAGC	249
Snezh	241	TCTCACTGTGGGACCTGCTGTTCCTGACAGGCATTGGGGCTGCGTGCTGCTGTGT	800
Sbjet	241	TOTCKCTGTGGGGACCCTGCTGTTCCTGACAGGCATTGGGGCTGCGTGCTGGGCCATTGT	808
Ouex2	301	GACCATCCTACTACGGAGTGATCAGGAGCCACTGTAGCAAGTGCAGGTCAGTCCTGGGGA	360
Spjet	303	GACCATCCTACTACGGAGTGACCAGGAGCCACTGTACCAAGTGCAGCTCAGTCCCGGGGA	360
Query	361	CTUTCGACTITISGTGTTGGACAAAAACAAAAGGAAACGTGGAAGGTGCTGCTGCTCCTCACG	420
ಶಿಜ್ಚಾತ	367	CTCTCGACTTTTGGTGTTGGACAAGACAGAGGGAACGTGGTGGTGTGTGT	420
GnetA	421	CICCAACGCCAGGGTAGCAGGGCCCGGGCTGTGAGGAGTATGGGCTTTCCCCAGGGCTCTGGC	480
Sbjet	421	CTOMARCHOMAGGETRGUAGGGCTCGGCTGTGAGGAGGATGGGCTTTCTCAGGGCTCTGGC	480
Grath	482	SCACTCRGADITGGRISTGGGAACCGCGGGCDCCAACCGCACTGGGGCTTCITCTGGGT	840
გაგის	481	GCACTCAGAGCTGGATGTGCGAACCGCGGGGCGCCAACGGCACAEGGGGCTTCTTCTGCGT	840
Query	541	GRACGAGGGCGCTCTGCCTCTGGCTCAGCGGTTGCTGATGTCATCTCTATGCGACTG	600
Sbjet	541	SGACGAGGCCGGTCTQJCTCTGGCTCAGCGGTTGCTGGATGTCATCTCTGTATGCGACTG	€00
Query	601	TCCTABAGGCCGATTCCTGACTGCCACCTGCCAAGACTGTGGCCGCAGGAAGCTGCCGGT	660
Sbjet	601	TOTAGAGGOOGATTOTTGACTGCCAGTGCCAAGAGTGTGGGCGGCAGGAAGCTGCOGGT	660
Query	663	GRATCOCATTGTGGGGGCCAGGRCAGCAGCCTGGGAAGATGGCCATGGCAGGTCAGCCT	720
Sbjet	662	SWATCOCKTTUTGOTGUGCCRGUACAGCAGCCTGGGAAGATBGCCATGGCAGGTCAGCCT	720
Query	721	GCGTTATCATGGGACCCCCCTCTGTGGGGGGATCCCCTGCTGTCCGGGGACTGGFTACTGAC	780
Shjet	721	GCGITALGATGGGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	789
Query	782	CGCTGCACRCTGCTTTCCAGAGRAGCAGCGGGTCCTGTCTCGGTGGCCAGTLTTTSCTGG	840
Shjet	781	CSCTSCLCACTOCITICCLGAGAGGAACCCGGTCCTGTC108GT0900AGTATTTGCTGG	840
Query	841	TOCTGTAGOCOGGROSTCASCTCATGCOGTGCTGGGGGGTTCAGGCTGTGATSTATVA	900
Sbyct	841	TOTISTAGOCCOGRACCTCACCTCATGCCGTGCAGCTGSGGGTTCAGGCTGTGATCTATCA	900
Query	901	TGGGGGCTACCTICCCTTTCGAGACCCTACTATCGACGAAAACAGCAATGACATTGCCCT	960
Sbjet	901	TEGOSSCIASCITESSITESGAGGCCTRSTATSGAGGAGAGCAGCAFGACATTGCCCT	969
Query	961	SGTOCACCTCTCTAGCTCCCTGCCTCTCAGAGAATAGATCCAGGGGGTTTGTCTCCCTGC	1020
Sbjet	963	GUTOCACUTETCTAGETCCCTGCCTCTCACAGAATACATCCAGGCGGUTTGTCTCCCTGC	1028
Querl.	1021	TGSGGGCCAGGCCTGGTGGACGGCAAGGTCTGTACAGTGACCGGCTGGGGTAACACACA	1090

```
White 1021 FORGOGREAGOCCEFGGTGUACOGCAAGGTCTGTACAGTGACCGGCTGGGGTAACACACACA 1080
Query 1981 GITCTATGCCCAGCAAGCTGTGGTGCTCCAAGAGGGCCCGGGTCCCCATCATAAGCAACGA 1148
Shipes 1081 GTF0TATGGCCAGCAAGTTGTFGCTGCFTCAAGAGGCCCGGGTCCCCATCATAAGCAACGA 1140
Query 1141 AGTITGCRACAGCCCCGRCTTCTRCGGGARTLRGATCRAACCCARGATGTTCTGTGCTGG 1200
           AGTTIGCHACAGCCCCGACTTCTACGGGAATCAGATCAARCCCAAGATGTTCTGIGCTGG 1200
Sbjot 1141
Shige 1202 CTATCCTGAGGGTGGTATTGRTGCRTGCCAGGGTGACAGGGGAAGGCGACTTTGTATGTGA 1280
Query 1261
           GUACAGAATCTCTGGRACATCRAGATGGGGGCTCTGGGGGCATTGTRAGGTGGGGTAGGGG 1320
Sbict 1261
           GGACAGAATCTCTGGAACATCAAGATGGCGGCTCTGCGGGCATTGTAAGCTGGGGTACGGG
                                                                  1320
Query 1921 CIGISTITIFGCCCGGRAGCCGGRAFTGIACACCRARGTCRIIGRCIICCGGGRAGIGGRI 1880
Sbjct 1921
           CTGTGCTTTGGCCCGGGAGCCGGGGGGTGTACACCAAAGTCATTGACTTCCGGGAGIGGAT
Query 1981 CTTCCAGGCCATAAAGACTCACTCCGAAGCTACCGGCATGGTAACTCAGGCCTGAGCCCG 1440
Sbirt 1881 CITCCAGGCCATARAGACTCACTOTGAAGCTACEGCATGGTAACTCAGCCCTGACCCCG
                                                                 1440
Query 1441 COTORTOGCOTOCTCCSCSCTOCTCCAGCATCCAGASTCAGASTTGGTCTGGTGGCTCCA 1500
Bb1et 1441 CUTCATOSOCISCIOCOGUGUTGOTOCAGCATUCAGAGTCAGAGTTGGTCTGGTGGCTCCA
                                                                  1500
Query 1801 GCCGCACGTGGCAGGCTCCACACTGGGCCTCACATGGAACGGTTTTCTGCTCGGATCCAG
                                                                 1560
3bict 1501
           GCCGCRCGTGGCAGGCTCCACACTGGGCCTCACATGGAACGGTTTTCTGCTCGGATCCAG 1860
Query 1961 TOCATAGATCCARGGATGCTGGGTCCRAGGACCTCTCCACRGTGGCCGGGCCCRCTCR
                                                                 1623
Shigt 1861 FORTAGATORAGGATGCTGGGTCGAGGACCTCTCTTCGACAGTGGCGGGCCACTCA 1620
Query 1621 ATCCCAGGGCCATTGGCCTCACCCTCCCACCCCATGTAAATATTACTCTGTGCTCTGGGG 1680
Shick 1821 ATCOURGEGOURTTGGCCTCRCUCTCCCACCCCRTGTRARFATTRCTCTGTCCTCTGGGG 1688
Ouerv 1681
           GCTGCTTTCGAGGCGCCCCTTGTGCGGATGCTCTTTAAATAATAAAGGTGGTTTTGATT 1739
CPG time:
          0.52 wser secs.
                              0.00 svs. secs
                                                   0.02 total secs.
Lambda
         8
         0.621
  1.33
                   1.12
Gapped
          K H
Lambda
         8
   2.33
```

Matrix: blastn matrix:1 -2 Gab Penalties: Existence: 6. Extension: 2

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Number of Fequences: 1
Humber of Hirs to DB: 452
Humber of Hirs to DB: 452
Humber of successful extensions: 1
Humber of successful extensions: 1
Humber of sequences better than 10.0: 1
Humber of HBP's gapped: 1
Number of HBP's gapped: 1
Hangth of query: 1738
Langth of query: 1739
Langth of query: 1742
Effective Length of query: 1712
Effective Length of query: 1716
Effective Lengt
```

Exhibit 2.



Length = 1781 (1 .. 1781)

Sequence 2: gi6680266 ref.NM 008281 13Mus musculus hepsin (Hpn), mRNA Length = 1781 (1 .. 1781)



NOTE: Buscore and expect value are calculated based on the size of the iir database.

NOTE if protein translation is reversed, please repeat the search with reverse strand of the query sequence.



Spjas	121	AAACCP-CRECATCICCSGCBAACCCCAGGGTTCCGCCCCAGCCCAACRGGTCARCCTGS	183
Query	181	BAATCATTARCAAGAGICCCIGACATGGCGAAGGAGGGTGGCCGGACTGCAGCATGCTGC	246
Shjot	191	SANTCRITRACEAGRATICCTGACATGGGGAAGGAGGGTGGCCGGACTGCAGCATGCTGC	249
Query	241	TOTAGROCCARGGEGGNOCTOTCATIGTGGGIACOTTGCTGTTTCTGACAGGCATTGGG	350
Shjet	241	TOCKBROCCARGETSGCRECTCTCATTGTGGGTACCCTGTTCCTGACAGGCATTGGG	320
Query	361	GEOGRAFICETORS/CATTGESACCATOCTA/TESCAGAGIGACCAGGAGCACTGEACCAA	340
Sbjet	301	BCCBCGTCCTGGGCCATTGTGACCATCCTACTGCAGAGTGACCAGGAGCCACTGTACCAA	365
Query	361	ergcagctcagtcaggggactcacgactrgcagrgtrsgacaagacggacggtacgrg	420
Sbjos	3€1	9TG/AGTTCAGTTCAGGGGACTTCACGACTTGCAGTGTTGGACAGACGGAGGGTACGTGG	429
Cnezh	431	AGGCTACTETECTCCTCACGCTCCAATCCCAGGGTGGCAGGCTCGGCTGTGAGGAGATG	489
9 b jet	421	AGGCIACESTECTCCTCACGCECTAATGCCAGGGIGGCAGGGCTCGGCTGTGAGGAGATG	459
Query	451	GGCIITCTCAGGGCTCTGGCGCACICGGAG:TGGATGTGCGCACIGCGGGCGCCAACGGC	540
Shiot	481	GCTTTCTCAGGSCTCTGSCGCACTCGGAGCTGGATGTSCGCACTGCGGGGCGCGAACGGC	540
Query	541	ACATOGOSCITCITTECCTGSACGAGGECGGACTSCCICTGCCTCASAGGITGCTGGAT	600
Sbjet	541	ACATCGGGCTICTTTTGCGTGGACGAGGGCGGACTGCCTCTGGCTCAGAGGTTGCIGGAT	609
Costl	601	STCATCICIGIATGIGACTGICCIAGAGGCCGATICCIGACTGCCACCIGCCAAGACTGI	€€3
Shjot	601	STCATCICIGIATGIGASTGICCTAGAGGCOGATICCTGACTGCCACCIGCCAAGACTGI	663
Query	€€1	GOCCGCAGGAAGCTGCCGGTGGACCGCATTGTGGGGGGGCCAGGACAGCAGTCTGGGAAGG	720
Shjet	661	SSCCSCASGARGCTSCCSSTSGACCGCATTGTGGGGGGCCAGGACAGCAGTCTGGGAAGG	720
Query	721	TOGCCGTOGCAGGTCAGCCTGCGTTATGATGGGACCCACCTCTGTGGGGGGGTCCCTGCTG	750
Sbjet	721	ISSCCOTOGORAGETCASCCTGCOTTATGATGGGGACCCACCTCTGTGGGGGGTCCCTGCTG	780
Caery	781	ICTGGGGACTGGGTGCTGACTGCTGCACATTGCTTGCCAGAGCGGAACTGGTTCCTGTCT	940
Sbjas	781	ICTOGOGACTGOGTGCTGCTGCACATTGCTTTCCAGAGCGGAACCGGGGTCCTGTCT	340
Caeza	341	JegresceagtatifecteglectetAccccGeAccicAccccatgcTgTgCAAcCgGeG	300
Shjet	841	COSTSGCGAGIAITTGCTGGTGCTGTAGCCTGGACCTCACCCCATGCTGTGCAACTGGGG	950
Query	901	STICAGGCTGIGATCTATGAIGGGGGCTACCTTCCCTTTCGAGAGCCTACTATTGACGAA	9-68
Sbjot	901	GITCAGGCTGIGATCTATCATGGGGGCTACCTTCCCTTTCGAGGACCCTACTATTGACGAA	960
Query	961	AACAGCAATGACATIGCCTT9GTCCACCTCTCTAGCTCCCTGCCTCTCACAGAATACKTC	1020
Shict	961	AACAGCAAIGACATIGCCTTGGICCACCICICTAGCICCCTCCCCTC	1020
Çuery	1021	CASTCASTSTGTCTCCCTSCTGCSGGACAGSCCCTGSTSGATSSCAAGSTCTGTACTGTS	1030

Sbjet	1001	CASCCAGISTGICCCCCTGCTGCGGGACAGGCCCTGGIGGATGGCAAGGTCIGTACTGIG	1080
Query	1581	ACCOGCTOGOGTARCACACAGTTCTATGGCCAACAGGCTATGGTGCTCCAAGAGGCCCGG	1140
Sbjaz	1081	A:C99C16G96TACACACAGTTCTA16GCCAACAGGCTA1G6T9CI:CAAGAGGCCC5G	1140
Query	1141	STICCCATCATAGGCAACGAGGTTGCAACAGCCCGGGGTTCTACGGGAATCAGATGAAG	1200
Sbjot	1141	STPCCCATCATAGCAACSAAGTTGCAACAGCCCGACTTCTAGGGAATCAGATCAG	1200
Query	1201	CCCAAGAIGEINTGIGCTGGCTATCCTGAGGGTGGCATTGATGCGTGCCAGGGCGACAGI	1260
Sbjet	1201	COCAAGATGICCIGCTGGCTACCTGAGGGTGGCATTGATGCTGCCAGGGGACAGT	1160
Query	1261	egaeggccctiteretgteaagacagcatcictgegacarcaaggregceectatereec	1300
Sbjot	1261	G0A00CCCCTTIGTGTGTUAA0ACAGCAICTCLGGGACATCAAGUTG0CG0CTATUTGGC	1320
Query	1321	ATTSTARGCT@GGGTACCGGCT@TGCTTTGGCCCGGGASGCCA@GAGTGTACACCAAAGTC	1380
Sbjot	1921	ATTSTARGCT903GIRCCS9CT9T9CITT99C0CCGSAASCCRGGAGISTACACCARAGT	1380
Query	1381	ACTGACTTCCGGGAGTGGATCTTCAAGGCCATAAAGACTCACTC	1448
Sbjet	1331	ACIGNUTICOSGRATEGATOTICARGOCCATARGACTOCACICOGRAGOTAGISGCATS	1440
Query	1441	GIBACTCASCOTTGATCCCGCCICATCTCGCTGCTGCTGCTGCTACTAGCATCCAGAGTC	1500
Sbjot	1441	elevines de la constitución de l	1500
Query	1501	NEAST ISSUETESTSSCIEGASCOCCASTSGIAGSCICCACACTGGSCOTCACATGGAA	1560
Sbjot	1501	ASASTTOSTETSSTSOCIECASCOTCAGGTGGIAGOCTCCACACIGGGCCTCACAIGGAA	1560
Query	1561	IGGTTTCCTGCTCAGATCCAGTCCAGGGTCCAAGGATGCTGGATCCAAGGACTTCTCTT	1625
Shjet	1561	TESTIFCCTGCTCAGAICCAGTCCACGGGTCCAAGGATGCTGGATCCAAGGACIECTCTI	1628
Query	1621	CACASTGUCCSGCCCACTCAATCCCAGUGCCATTGGCCTCCACCCTCCCACCCATGTAA	1688
Shict	1621	CCACAGIGGCTGGCCCACICAAICCCAGGGCTATIGGCCTCACCCTCCCACCCCAIGIAA	1669
Query	1681	ATAITAITCTGTGCCCCTGGGGGGCCCCCTAGGGAGCCCCTTGTGLAGATGCCCTTLAGAT	1740
Sbjot	1681	ATATIACTCTGTCCCCTGGGGGGCGCCCCTAGGGAGCCCCTTGTGCAGATGCTCTTTAAAT	1740
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Sbjot	1741	AATRAAGGTGGTTTTGATTAATGGGAGARAAAARAAAAA 1781	

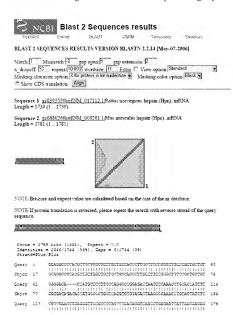
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CFU time: 0.02 user sees. 0.01 sys. sees 0.03 total sers.

Lembon F H
1.33 0.621 1.11

Gapped
Lambon K H
1.53 0.621 1.12

Matrix: blestn matrix:1 -2
Oasy Pensities: Existence: 5, Extension: 2
Number of Sequence: 1
Number of Sequence: 1
Number of Sequence: 1
Number of Sequence: 1
Number of successful extensions: 1
Number of SEP's suppost 1
Number of SEP's suppost 1
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Length of green; 1781
Length of green; 1781
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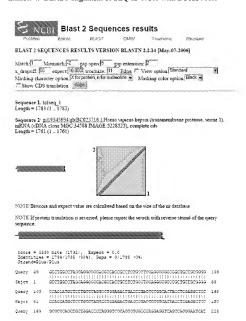
Exhibit 3. BLAST alignment of rat and mouse hepsin coding sequences



Skjet	137	$\tt CUGGGAAGGGGTAGGGGTGGGGGGGGGGGGGGGGGGGGGG$	296
Query.	177	PTTTTSACATOGCCCARGUAGGGTGGTTDTSACTTCACCCTGCTGTTTCAGATTTAAGGTTG	238
Sbyst	197	TOUTGACATGOCEAACGACGGTGGUGGGCTGCACCATGCTCTTCCEGRUUCAAGGTGG	25€
Query	237	CASCISTIACPOTOPPARACOTOTISTICCISACROSCRITOPPOSCIOCUSCOSSICA	256
Shjer	257	CASCIVICATIONSGRACCONSCRIPTOCTOACAGGGCASTGGGGCCSCGFCCT999CCA	318
Query	297	TIGUGAGCATOCTACIACUSAGUAGUAGCAGCUGUAGUAGUAGUAGUAGUAGUAGUAGUAGU	35€
Skjet	317	FIGURACIATOCTECTOCAGEGTGECCEGGEGCCECTFECCERGTGCEGCTCEGTCLEG	376
duerl.	387	ODGACTOTOGACTTTIGGIGTIGGACAAGACAAGAGGGAAGGTGGAGGCTGCTGTTTTTTTT	41€
Saget	377	GAJACICASSACITYCASTVIIOGACAAGACGGAGGGTACGIYSTAGOCTACIGIGCICCI	435
Guery	915	CACSCICEAAPPDIAGGGCAGGGCTCSGCTSTSAGGAGAAAPGGCTTTCTCAGGGCTC	476
Sbjet	437	CATOTTCCAATGCCAGGGGGGGGGGGGGGGGGTGGGGGGGGGG	498
Query	477	TOSCOCACTCAGAGYTPGATGTGCGGAGCGCGGGGGGGACGGYTACATCGGGGCTTCTTCT	838
Skyst	497	TOGGSCACTOGGAGOTGGAGTGCGCACTGCGGGCGAGOGGCAACATCGGGCCTTCTTTT	554
Ø×ez7.	537	909799ACGAGGGCGGCCGGCCT99CFT49CGGTTGCTGGATGTCKTCTCTGTAT9CG	5.9 <i>E</i>
Spict	557	BOSTONACGASGSCEGACTSECTTEPPOTOANACGETGCEGGATETTATCTCTNTATGEG	878
Çuery	597	ACTG/FCTAGAGDCCGATTCCTGACTGCCACTGCCAAGACTGTGCCAGGAGCTGC	656
Spics	£17	ACTOPTOTAGAGGCCGATTCCTGACTGCCACTTGCCAAGACTGTGGCCGCAGGAAGCTGC	678
Эзегу	663	CUSTGGRTCSCATTST9999000CAGGRCGCGGCCTSSGAAGAT90CCATGGCAGGTCA	716
Mojet	677	COSTGGREEGCATTST99990GCCAGGACAGCAGICT99GAA96T9GCCGTGGCAGGTCA	736
Query	27.2	OCCTOCGTEATGRIGGGACCEACCECTGTGGGGGACCCCGGCTGTCCGGGGACCCGGCACCCACC	778
Swict	222	OCCTGCGTTATGATGGGACCCACCTCTGTGGGGGGGTCCCTGCTGTCTGGGGGACTGGCTGC	798
Greza	777	TURCUSCUSCRETOCTTTCCRSRGRGGRGCOSSGTCCTGFCFC9GTGGCGRGTATTTG	539
Spjes	757	TRACTOCTGCACATTGCTTTCCCAGAGCGGAACCOGGTCCTGGCTCGGGTAGCGAGTAFFTG	388
Query	527	CTRETOCTORECCOSGROCTOROCTURE O'CONGROCTOROCTOROCTOROCTURE O'CONGROCTOROCTURE O'CONGROCTOROCTURE O'CONGROCTOROCTURE O'CONGROCTOROCTURE O'CONGROCTOROCTURE O'CONGROCTOROCTURE O'CONGROCTOROCTURE O'CONGROCTOROCTURE O'CONGROCT	895
Shjet	85"	CTGGTGCTGTAGYCCOGAACCTCACCCCATGCTGTGCAACTYGGAGCTTGTGAECT	316
\$4423.	897	APTAT99999TACCTTCULTTTCGAGACCTACTATCGACGAAAACAGCAATGACATTG	356
Sbyet	917	atchtuggggethectftcctfttcgacaccctactaftgacgaaaacagcaatgacattg	978
Query	867	CCCISCICIACOPYTTAGOTCOCCCCCCCCCACAGARIADATOCAGCCGCTTGCCCCC	1016
Sb) ರಾ	977	OTTP90TOCACCTCTCTAGCTCCCTTROTTCTCACAGAGACACCCAGCCAGTGTSTCTCCC	1036
Çuery	1017	CTGCTGCGGGCCGGCCCCFGGTGGACGGCCGGCTGGGGTACAGCAGTGACGGCTGGGGTAACA {}}{}	107€

Stycz	1037	$\tt TPSTFOCOGRAGGUCCTGGTGGATSGTAAGGTTTGTACTGTGACCGGCTGGGGTAATA$	1338
Query	1077	CROROTTOTATGGCUASCASCISISSISCECCARORGGCCCGGGTCCCCATCATRASCA	3136
,335 j e t	1097	CRCRETTETATESCORRORGOCTATGGTGCTCCARGAGECCCSPSSTTCCCAFCATAAGCA	1156
Ouer.	1137	ACCAMENT PECHACAGGCGGACTICTADOCCAAPCAGAT GRAGGCGAAGATGTTCTGTG	1196
Shipet	1157	AGGRAGTTTGCARCROTCCCGACTTCTACGGGRATTRGATCAROTCCAAGATGTTCTUTG	1216
Szezh	1197	CTUSCIATORISMOSPISSTATIGATSCRISCCASSSIBACAPISSASSOCICACTITISTA	1156
Sbjer	1517	TPOPOTATOCTGAGGUIGGGATTGATPOOTOOCKOOOCGAGAGGGGGGAGGGCCCCTTTSTOT	1276
Quecy	1257	STURGURCAGRATCTCTGGAACATCRAWRIGGUGGUTCTGGGGCATTGTAAGTTDGDFRE	3336
Sbjet	1277	organia-cascatuto-eggacatuan-eggisorgati-eggaci-eggaci-egggia	1836
Querr	1317	CSSPCTGFGTTTTGGCCCGGGAGCCGGGAGTGTATACCAGAGGCATTGACTTCCGGGAGT	1976
Enjor	1537	DOSPOTOTGCTTIGGCCCGGAAGCTADGAGTGTACACCAAAGTCACTGACTTTTTGGAAGT	1338
Query	1877	SCRICTFOCROSCORTALAGACTCACTCCGRAGGTADOSSCRISTALTCAGGCCCTGAC	1436
Sbjet	1397	OGRFTTPTMAGGCCRTARAGACTCRGTCCGAAOPTMGTGGCRTUGTGACTCAGCCCTGRT	1456
Coera	1497	CCCGCCCCATCSC-CT9CTTC9CGCTSCCCCAGCATCCAGAGTCAGAGTT9GTC19GTGG	1698
Short	1487	CCCGCCTCATCTCSCT9CTCCGTGCTGCACTAGCATCCAGAGTCAGAGTTGGTCTGGTGG	1616
Query	1456	CTOCAGOCGTAGGTAGGTAGGTAGAGGTTAGGAGGTTTTGTGGTAGGTTAGGAGG	1585
Seget	1527	CTCCAGCCCCACGEOGIAGGCIDCACACTGGGCCTCACATGGAAIGGIIICEIGCTCAGA	3576
Onest	155€	TOTASTETATAGATOGAAGGAJGOTGGGTCCAAGGATCFCTTTOGAGAGGGCCGGCCC	1615
303cc	1577	TOTASTOCARGOSTOCARGUATGUTOGRITOTAAGSKUTTUTUTSUCKURGIGGUUGGUUS	1636
Query	1616	ROTORATGGGROGGCTATT9995TGAGCCTGGGAGGGGRTGERAA7ATTAGTGTGTGTG	1675
Shjet	1637	ACTCAATSSSAGGOCATTOGOCTCACCCTCCCACSSCATGIARATATTACTCTGTCCTC	1656
được,	167€	TGGGCGCTTCTTTCGGGGGGGCGCCCTTGTGCGGGTTCTTTTTT	1735
Sejet	1687	TGGGGGGCGUTCTRS-GGRGCCCCTTGTGCRGATGCTCTTTARRTARATARAGGTGGTTTT	1788
Query	1736	GATI 1735	
20200	1786	GATT 1789	

Exhibit 4. BLAST alignment of SEQ ID NO:1 with BC025716.1



121	PRODUCESCUTSCUTSGROUNDERFORMUND CONTROL OF THE PRODUCE OF THE PROD	180
223	TARCHAGRAGGUAGTSATER99090AGRAGGAGGGGGGGGGGGATT9T900ATGCTGUTGCA	288
381	TARCHAGA:00CAGTGACATUGGGGAAAGAAOOTOOCCGACTGTGGGCATGTTOCTCCA	240
289	CACCTRAGGTGGCAGCTCTCACTGCBBBGACCCTGCTACTTCTGACAGCTATCGGGGGGGGG	348
241	GROCCRAGGIGGCAGCICTEACTGCGGGGGGCGCTGCTACTICTGACAGCCATCGGGGGG	300
349	CATOUTPEDTTATTOTOGCTGTTUTOCTCAGEASTGATTRGGEGGGGGGGTGTACTCAGTDT	408
301	CAPOSTPOSOCIATEGEGGEGTICTOSTEROGRAGGAGGAGGAGGGGGGTGFADOCRGTPG	360
403	APOTCAGCICISCSCACOCTOPOTCATGGTCTTTGRCARCROPSARPOGRCGTGGCGGC	468
361	AGGTCAPCICIPGSGEUUTOGGCTCATGGTCIITGACAAGEUGGAGGAGGAGGTCGGCCC	420
469	TSCTSTSCTCCTCGCGCTCCAACSCTASGSTEGCCGGACTCAGCTGCGAGGAGGAGTAGCAC	828
421	TOCTGTGCTCCTCGCGCTCTAATGCTAGGGTAGCCGGACTCAGCTGTGTGTG	480
829	TOOTON 9990ACTGACCCACTCUGAGCTGGACGT9CGACGGCGGGGGGCGACGGCGACGGCAACGG	5.83
481	PETERSONAL TERRETERS CONTROL OF THE PROPERTY OF THE PETERSON O	8.80
633	COGGCTTCTTCTGTGT99AC9AGGGGGGGGGCTGCCCCACAC9CCAGAG9CTGCTGGAGGTCA	443
8-61	CGGGCIPCTTTTGTGTGTGTGTGTGGGGGGGGGGGGGGGG	600
649	TOTORSPRIETGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATGTGCGAGACTGTGGCC	708
601	TCTCCGTGTGTGATTBCCCCCAGAGGCCGTTTGTTGGCCCAFCTGCCAAGACTGTGGCC	560
7-33	GUAGGAAGUTDERUGTUGAUUGURTUGTGGGAGGUTGGGAUGAUUTTGGGUUGGTGGU	768
867	PCAGSAN-CTGCCCGTGGRCCGCATCGTG993A00CCGGGRCACCRGCTTG295C090106C	720
769	OPTOGURAGIUAGUUTICOCTATGATGIRGGRCACUTUIGI999996ATGCCTGUTCICUG	828
721	CGTGGCAATTTAGCCTTUGUTATGATGGAGCACATCTCTGTGGGGGAATCUCTGCTCTTTTG	780
829	GGGACTP97FPUVGACAGCCGGCCACTPGTTCCCGACAGCGGAGCCGGTGTTTTCCCGAT	888
731	GGGACTGGGTGCTGACA9009000ATTGCTTCCCGGAGCG9AG0099GTCCTGTCCCGAT	540
839	GGCGRGTGTTTGTCGGTGCCCTGGCCCAGGCCTCTCTCTCCAGCTGCAGCTGCGGGGTGC	348
841	DECEMBETOTTTGCCGGTGCCGTGCCTCTCCAGGGTCTGCAGCTGGGGGGTGC	500
549	AGCTITEGELIACCACEDEPPTATCTTCCCTTTCGGGACCCCAACACCGGGGGGGACAC	1009
931	AGGCTGTGGTCTA9CAD9999GCTATCTTCCCTTTCGGGACCCCAACAGCGAGGAGACA	560
1005	GUARDHATHT9600TEGTUCACCTTTDUMTD00CT600UUTCMCMRATAURTDUMA	1068
961	SCHOOLS AS A CONTROL OF THE CONTROL OF THE CONTROL OF THE CASE OF	1020
3069	CIGISTSCTTCTTAGCIGCUGACCAGSCCCTTGITTGATGGCAAAAICIGTACCGTGACCG	1128
	228 181 249 241 349 301 408 301 408 409 421 549 601 708 881 882 881 882 881 882 881 882 881 882 883 884 884 884 884 884 884 884	

Stages	1021	DISTORGED COCAGE ISC 1990 DASSOCOTOS GAS AGAINS FOR SANOR GAS GAS	1550
Query	1129	GOTGGGGCARCACGTAGTACTRINGCCRACAGGCCGGGGTACTCCAGGAGGCTCGAGTCC	1188
Stojet	1081	PCT9999CARCRUSURGERCTATG9CTARCAGGCCGGGGTRGTCCR9ERGTCT9GRGTCC	1140
Gretz	1155	PCATALTORGARIGATETETECEMP9000CTQACTTGTATBURRAPCM9ATCRAGGCCA	1245
Statet	1141	OCRTRATORGOARIGATETOTERATEGOOGOTERCTICTATEGRAROCAGATORREGOOGA	1255
Guezy	1049	AGAISTITTAFALTGACTACCCCGAGGGTSPCAITAAGACCTGCCAGGGGGATAPLDAFA	1308
Shjet	1201	AGATGTTCTGTGCTGGCTACCCCGAG9GTGGCATTGATGCCTGCCAGGGCGACAGCGGTG	1250
Quecy	1908	GICCCTITGTGTTDAGGACAGCATCTCTCGGGCCCTAGGTTGGCGGCTGTGGCGTTG	1363
Mojet	1261	GECCCTITETOTOTOROGANAGCATCTCTCPGRACOPCACOTTGGCGGCTGTGTGHCATTO	1320
Query	1165	TOANTTGOGGCACTEGTISIPTOCT9900CRGRAGUCRGGCSTCTACROCRARGTCRGTG	1415
Seget	1921	TWANTINGOGCACTOSCITISCOCTOGCCCAGARGCCAGSCSITIACACCARAGTCAGIG	1899
Query	1429	actificoscrutoradical inaacactorotocgrascoscocatestor	1488
spias	1351	actiogoggagiggaictiduropotaimaagaudurciuugragduropoporisgiga	1445
Query	1469	JCUNBCTCTGRC1992T99CTTCTGGCTGGGCABCCTTCTA999CCCGAGGTGATGGCDGTG	1548
Skjet	1441	CCCADETEPARODOSTGCCTTCTCCCTGCGCAGCTTCCAGGGCCGAGGTGATCCCGFFA	1500
gaerr	1549	SINGSAICCROACIGGGCGRAGRATUPSACGITITICTTCTTGGGCCCNGTCCACAGGIC	1608
Sbyst	1501	GEGGGATCCACGCD999000A4GAT4GGACGTTTTTCTTTGGGGCCGGATCCACAGGTC	1560
Query	1809	CRASSACACOTTOTOCOMOGETCUTCTCTCTCTCACAGTOGGGGGGGCACTCAGGCCCCAG	1868
3,07 cr	1861	TAAPGAGAGGGTCCCTCCAGDDFFOTFOTFOTFCGAGAGTGDCGGGGCCCGAG	1620
Query	1669	ACCRCCCARCCTCATCTTCTGACCCCCATGTRAGTATTGTTCTGCTGGCACTCCT	1728
Mijet	1621	ACCAPPERACUTORCCUTGRECCCCATGIRRATATTGTTCTGCTGTCTGGGACFCUT	1660
Steri	1729	SPITAGGIGUCUCIGATGATGGIGATGCICTITARATARIARAGATGGIIITGATT 1788	
Singet	1681	GTCTRGGT9CODTT9ATGATGHGRIGCTGTTTRAATAATAARGRT9GTTTTGATT 1735	

Exhibit 5. BLAST alignment of SEQ ID NO:1 with NM_182983.1

Blast 2 Sequences results	
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]	
Match Mismatch 2 gap open 3 gap extension: P	3
Sequence 1 icliseq_i Length = 1783 (i . 1783)	
Sequence 2 <u>uB3399114-nerPNM_181953_1</u> ;Homo sapiens hepsin (transmembrane protease, (HPN), transcript variant 1, mRNA Leight = 2365 (1 2365)	serine 1)
NOTE Bitscore and expect value are calculated based on the size of the in database.	
NOTE if protein translation is reversed, please repeat the search with reverse strand of the quegrence	nery
And the second s	
Score = 2053 bits (1559), Expect = 0.0 Identifies = 1558/1588 (1009), Gaps = 9/1589 (E4: Strand=Plue(Plue	
Quary 19: OFFCCCACCCTGSCCCAGGEOFTCAGCCAGGGAATCATTAACAAAMSSCAGTGACATGGC	250
Nyet 771 GUTCCGCCCTG9DCCS936GTCAGCGGGGATCATTAACAAGAGECHTGACCTGGC	880
Query 181 90A9AB98A6G476GCUGGACTSTSCTCATSTTSCTCCAGGACCCAGGTSGCASCTTCAC	210
Sb2:t =881 OCRGRAGIAGIGTGGCCGGRTT9T9CTATGCTGCTCCAGALCIRAGGTGGCR9CTTCTCAC	390
Query 311 ISCS9998/000760780770708CAGCCRTCGGGGGGGGGGCAT70706GCCAT7GTGGCTGT	376

Shoot	381	POCHEGEAGECTROTALITYTEA/APOCATOLOGICGEATACTROPROMITYTOPOTOT	950
Owers	371	TOTCCTTAGEAGTEACUAGTAGCCGCTGTACCCAGTGTAGGTTAGCTCTGCGGAGGCTCG	429
ಶಿಕ್ಷಕ	981	POTOTOROGRAFICAGGAGOCOCTETACCORSTGCAGGTCAGGTCTGCGGACGTTCG	1010
Query	482	OCTUATEGGEOTTIGACAAGATOTAAGGGACGTGGGGGGGGGGGGGTGCTTTTTTTTTT	490
Shirt	1011	SCICACGGICITISACAAGA/PRAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1070
Query	471	COCCA99GEAGCCGGACTCAGCTGCGA9GAGAT999CTECCTCAGTGCACTGACCCACT	550
Epget	1971	DENCAGATAGOOGGACTUASCTBOGAGGAGATAGACTTOCTCAGGGCACTGACCCACTC	1180
Coer.	8.6.1	CORCUTOGROSSOCIACOSCUGACIÓCARTOSCACOSOSCISTOTECTOTOTOGACER	670
29202	1131	CORPORDORACOTO CORRECONOGRACIO CORRESPONDENTO TO TO TO TO TO TO THE CORPORATION OF THE CO	1199
Query	611	SOURSCITCOCCACACACACACACACACACACACACACACACACACA	670
Shirt	1191	GOGGAGGCTGCCCCACACCCCAAAAGGCTGCTGGGGGCCATCTCCCATGTGTGTG	1250
Query	673	AGRACIOTTTVTTGGGGGCCCATCTGCCAAGACTTTTGGGAGGAAGGCTGGCCGGGGAAGG	780
80318	1251	ASSOCIATETTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1310
Coerl	731	CATCTT995A09CC995ACACCTACCTTGGGCC95T99CT59CAAGTCAGCCTTGGTA	759
80000	1311	CHICOTOPIAGOCCOGGACACCAGCTIGGGCCOGGTGGCCGCGAGGCAGCCTCGCCA	1376
Query	751	PARTGARGUACACCTCTGTGGGGGATDCCTGCTCCCCGGGGATGCTGGTGGTGATAGCCGC	920
Ebjet	1371	TGATSGASCACACCTCTATAVAGGATCCCTSCTCTCCGGGGGATTGAATACAGCCSC	1489
Smerk	861	CONTROLTOCOGRACCIONACCIOGGICCTGTOCCTATOGCCAGTUTTICCCGGIGCCGT	916
Suget	1431	COACTECTTCCCGGGGGGGAACT99051CCT0TCCCGGATGGCGGGTGTTTGCCGGT9CCCGT	1490
Spery	311	GCCCCAGGCTTTTCTCTACGGTTGCAGCTGGGGGTGCAGGCTGTGGTTTACCACGGGGG	970
86500	1491	PROCURSOCOTOTOCCCACGGTTTGCAGCTSROPRITACAGGGGGGGGGGGGGGGGGGGGGG	15.50
Query	971	OTATOTTOCCTTTCOGGRCCCCAACAGCGABBRARARCRGCAACGRTATTCCCCTGGTCCR	1030
3054p	1881		
	1001	CTRTC:TTCCCTTTODDUBOOUCARCAGCGAGGAGAACATCAACGATRITGCCCTGGTCCA	1615
Sowal.	1931	COTTTTCAGTCCCCTGCCCCTGACAGAATACATTCAGCTTGTGTGCCTGCC	1080
Split			
	1031	COTTOTAL PROPERTY CONTINUES AND A STATE OF THE STATE OF T	1090
Short	1931	CONTO TRATONON TROUGUTOR AGRANA ACRITICADA TOTO TO GOUTO COLASCITECTOS ANTICOLOS (COLOS COLOS CO	1090 1670
Short	1031 1611 1091	COTTOTAD PROPORTED DUCTE CACAGARTA CAPTULAD TOTO OF STOCK CAGACT GOODS 1111111111111111111111111111111111	1090 1678 1189
Sbjot Query Sbjot	1031 1611 1091 1671	COTTOT ASTRONO TROUDOTTA ANGRATA CATTLE POTTOTOTOTO COTTO CARGODO CONCUENTO	1090 1670 1189 1789

```
Title: 1791 CAATGGCGCPTRCTTCTATGGABACCAGATCRAGCCCAGATGTTCTGTGTTGGCTGGCTACCC 1880
Query 1271 CGAGGETESTATYGAFOCCTGCCAGGGGGAGAGGGGTSFTCYYTTYTTGTGTGAGGAGAG 1235
Query 1881 CATOTOTOGGROGO:ADSTIDADAGCTATATAGAGTTGGGGGTATTGGCTATGC 1890
Which 1911 CATCHCTCGGACOCTACGGTGGGGGGGTGTGTGGGGTTGTGAGTTGGGGTGGGGTGGGGTGGG 1976
Query 1891 OCTORCOLAGRAGICAGGESTETACATTARAGTCAGTGRCTTOLOGGRRSTGGRTUTTOTA 1460
Query 1481 GGTCATHRAGACTCACTCOGRAGGCAGGGGGTGAGTGAGTGAGTGAGTGAGTGGGTTC 1815
Sbjet 2981 PRTEMIARAJAUTURUTUGGRAGUGROUDGERFREFTREUURGUTUTURUUGGETGGUTIC 2999
SERVE COST TOSCIOCOCASCOTOCASGOCCUSAGOCGATOCCUSTOSTOSTOSTOCACOCTOGGCCUAG 1150
Query 1871 GATGGGAUGTTTTECTTUTTGGGCCCCGGTCCAAGGACACCCTCCCTTCAGGG 1880
Haget 2181 GATGGGROSTITTTCTTCTTD99000000TCCRCAGGTCCRAGGACRCTCTTDCTVDW996 2210
Sbjet 2211 TCCTCTCTTCURCRGTGGCGGGCCCACTCMGCCCGRGACCCCCAACCTCACGCTCCTG 2270
Quary 1691 ACCCCCATGTAAATATTGTTCTGCTGTCTGGGGGCCCCTGTCTAGGTGCCCCTGATGATGATGG 1780
Query 1781 SAIGCTOTFTARATARTARAGATGGETTTMAIT 1783
Shipt 2001 GATGUTUTTEAAATAATAAAGATFUTTTTGATT 2060
```

Score = 171 bits (193:, Expert = 4e-99 Identities = 199/193 (100%), Gaps = 0/193 (0%)

Exhibit 6. BLAST alignment of SEQ ID NO:1 with NM 002151.1





NOTE Bitwore and expect value are calculated based on the size of the nr database

NOTE. If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Sojet	121	POTCASSOCTSCASCASCASCASCASCASCASCASCASCASCASCASCAS	196
Query	191	POGROCCCAGGITCCCAGCCTGGCCCAGGGAGGFCAGCCAGGGGAATCACTAACAAGAGGCA	240
Shjet	191	TGGACCCCAGGGFTCCCCCCCCCGGGGGGGGGGGGGGGGG	246
Query	241	GIGATAT99000CAGARGGAGGGTGGCCGGACIGTOCCAT9CTUCAGACCCAAAGGTGG	200
ಶಿಶ್ವರಕ	241	STRACKFOOCGCAGAAGGAGGGTGGCTGGATTGTTGCAGCTGCTGCTGCAGACCCAAGGTGG	800
20esy	301	CASCICICACIDODODANCOTOCINCITOTERCAGACCATORROCOSTATOTOGOGOCA	360
Sbjet	303	CASCICICACIPOPOPOLACIOTACITCIGACAGCEATCODOPOPOLATIC/FUEGCA	3€0
Coery	3€1	TP97900T0TUTUCTCAGGGGGGCCE96890090T9TAGUCAGGGCAGGUCARCTCTG	42¢
abset	363	THOMOGUTOTTCTCCTCAGGAGTGAGUAGGAGCOGUTGTACCCAGTGCAGGTTAGGTGTA	420
Query	422	COTAGOTOROUTOSTOTTTGACAAGACEGAAGOEACOTOROUTOCTGCTCCT	499
Ebjat	421	OPEROGETOGUETALEGICITIERCHRENOPERAGORICETEGGGGGGGGGGGGTGCTGTT	480
Szezh	637	JGJGCTCCRACDTCADDTADCTGGGCTCAGCTGLGAGGAGATBODCTTTCTCAGGGCAC	840
8bjet	491	CHERCTCHARDSCHARRINGCOGGACTCAGCTGCGAGGABATSBSTTTCCTCAGGGCAC	846
Query	841	YGACCCACTCUGACCTGGACGT9CDAAC990909CGCCAATGGCACGTCCGGCTTCTTCT	600
Shist	843	THANCCACTOURAGETINGACTINCHARDSHOLDCHARDSCACTITY999TITCTICI	800
Query	103	GIGIGGACIRADGIADGCT90CCCACACCCAGAGGCTGCTSGAGGTCATCTCCGTGTGTG	260
Epjet	661	OPGFGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTCCGGTGFGTG	660
Spery	662	ATTGCCCCAGASSCCSTITCTT9SCCSSCCATCTGCCAAGACTGTGGCCGCAGGAAGCTSC	720
Sbjet	861	ATTROCCAGAGOCOFTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGCAAGAGAGCTGC	725
∂αsz2.	721	COTORACORCATOSTGGGASGCCOSGGACACTAGTT7009CCGGTGGCGGGGGAGGTCG	786
Short	721	CCGIGGACCOCATCSTOFSAOOCCAGGACACCAGCTIGGGCCGGTGGCCGFTGGCAAGTCA	780
Onesh	781	GCITTOSOTAPGAPPACACCCTCTGTGGGGGATCCCTGTCTCCOSSGACCTGGGTGC	840
Sbjat	3.27	OCCTTCGCTATGATGGAGCACACCTCTGTGOGGGACCCCTGCTGCGGGGGACTGGGTGC	840
Speck	341	TGACAGCUSCUCRCTSCTTSTSSGASUSGRACOGGTUUTSTCCCGATGSSGASTSTTTS	200
Sbjet	841	TEACASCODOCACTGCTTOCCGGRGUSGAACCBGGTCCTGTCCCGRTGGCGAGGGTGTTTG	990
Query	501	OCSTSGCGTGGCCLAGGCTGTCCCCAAGGTGCAGGTGGGGTGCAGGTGTGGTCT	360
Bajst	501	OCCOPROCOSTGGCCCAGGCCTCTCCCCCACCTGCGAGGTGCAGGCTGTGGTCTT	360
Query	961	ACCROSSODIRECTYCOCCTTYCOGGROCCCARCASCGASGASGASGARCGGGGGGGGGGGGGGGGGG	192
Sbjet	961	actacoposogriateteccetteogracederactaografia arcageratio	192
Spech	1321	COTOCOTOTACOTACTOTACACACACACACACACACACOTOTOTOT	108

წხვლ	1021	COCTOSTOCACUTURAS COCTOCTOCACAGAR TALATCUASCETSTSTSTCCCC	1080
Query	1991	THROTOLOGIC CROST DIATORIA DE TRANSPORTA CONTRA DE DESCRIPCIO DE TRACA	1140
Skjet	1081	CAGCIGODESCHASSONOFOGTGGATGGCANGATTISIAOOFTGAGGGGCTGGGGCGACA	114-3
01623	1141	THE ANTIAC TRESCUENCIA CAGGODORGEN CONTRACTOR DE RESCUENCIA DE RESCUENCI	1200
შხვდა	1141	oggasta teatuco ciarcas successos tativo appropriation to capital appropriation of the property of the prope	1500
Quezy	1201	ATGATGTTTGCAAT990977GACTTUTATGGARACCRGATCAA9000GARGATGTTCTGTG	1160
Skjet	1201	ASSAIGNSSEAT 990003GACTICTATGGAAACCAGATCAA9000CAAGATGTICTGTG	1263
Query	1761	CTGGCTACCCCGAGGGGGCAIFAATGCTTGCCCAGGGGGACAGGGGFGGTCCTTTGTGT	1320
Singot	1261	CIGGCIRCCCCGAGIGT97CAITGAIGCCIGCCAGGGCGATAGC9GTGCICCTIIGIGT	1320
Query	1321	STORAGE CASCATCTUTUGGE COCCACSTTOROGOCTSTUTGGCETTTGTGE TGTGAGTTOROGOC	1980
ಶಕ್ತಾರಕ	1371	STOROGRUROCATCICICIGREDITROFFF000000TOTGTGGCRTTBFBRGTT0900CR	1380
Query	1881	CIGGITFIDITCT9900CAGAAGCCAGGGGITTATACCAAAGTCAGTGAGTICCGGGAFI	1440
Sbjet	1881	CEOSTISISOTUTSGCCCAGAGGCCGGGGTTATCCCAGAGTCAGTGACTECCGGGGGT	1443
Çuery	1441	GRATCTTCCRGGCCATAAGACTCWCFGCGARGCCAGCGGCATGGTTAGGCGGGCTCTGAC	1600
Shirt	1441	GGATUTTOCAGGOTATAAAGASTCAUTCUGAAGCCAGCOGJAT93FGACCCAGUTCTGAC	1500
Query	1601	GGGTGGTTCTOXCT909(AGGCTCCAGGGCCCGAGGTXATUUUGGTGGTGGGATCCACG	1563
25293	1501	ONTYGOTTCTCGCTGCGCA9CCTCCW990000AGGTGATCCCGGTGGTAFATCCAGG	1850
Query	1561	CTGGGCCGAGGATGTGACTTTTTCTTCTTGGGCCCGGTGTACATGTGCAAGGGCACCCCT	1620
35505	1881	CT999979A9GATGGAACGTTTTCTTCTTCTP99GCCGGGTCCACAGGGTCCAAGGACACTCT	1610
Query	1621	CONTRAGOSTUTCICITICACASTSPS9900CACTCAGGGGGGAGAGCACCT	1880
Bhjet	1821	CCCTCERSSTOTFOFFOCRCAGTSGCGGGCCCACTCAGCCCCGAGGCCACCCCAACCT	1690
Query	1681	CACCITECTEACOUCHIGTARATATIGTICISCISTITEGGALTCCTGTCTAGGTGCCC	1740
Spjet	1481	CROCCTOCTORCCCCIRTHARAIAITSTTCTGCTGTCTGGGACTCTTTCTAGGTGCCC	1740
Query	1741	CIGATGRIGGGAFGIDYIYYARAYARTRARGATGGITTIGAYI 1788	
Sbjes	1791	CTOATGATGOCCATTICAARTAATAACATGCTTTTGATT 1788	

```
CEP time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lancid E B 
1.33 0.621 1.10

Rapped Lancid K H 
1.83 0.621 1.11

Montant bleath merchani - 0 
Supermiller of Requester | 0.03 total secs. 0 
Howher of Requester | 0.03 total secs. 0 
Howher of Requester | 0.05 total secs. 0 
Howher of Represent Secs. 0 
Howher of Repre
```

Exhibit 7. BLAST alignment of SEQ ID NO:1 with X07732.1

		Blast	2 Seque	nces res	ults		
194	ASSOCI	Entrez	SLAST	Chart	Toxosemy	Southern	
BLAST	1 9E	QUENCES RES	ULTS VERSIO	ON BLASTN	2.2.14 [May-87-	2996]	
π_drop Maskin	off [50 g char w CDS	Mismistch, [2] expect [0.00] acter option [X for i translation [As	X wordsize: 11 protein, n for nuc	Filter C V	new option Star	dard on Black	7
		cliseq_1 3 (1 1783)					
		pi32063/embiX07 3 (1 . 2363)	732 LHomas h	epatoma mRN	A for serine prot	esse hepsiu	
			a de la companya de l		1		
NOTE.	Bitsco	re sud expect vals	se are calculated	based on the	size of the ar dat	sbase.	
NOTE		ein translation is s	reversed, please	repeat the sear	ck with reverse	strand of the q	uery

Ident	ities	63 bits (1593) = 1698/1693 (s/Slus	, Zopert = (195%), Gaps =	0.0 • 0/1893 (0%			
Query	191				attracargassc:		250
Bhjet	771	GGICCCACCCIG	DOCCADOADAYA	GCCRGGGRATC	atiaacaagapgti	STURCETOGO	830
Swez3.	251				DAGA/DOTAA/GGTG		210
Signet	381				CAGACCCAAGGTG		390
Query	311				RECATECTERE		370

Shjet	893	TGCGGGGACCTTGCTGACAGCCATCGGGGCCATGGTGGGGCCATTGTTGGTTG	880
Query	372	${\tt INTOCTCROORSTORCCRGGASCISCTSTROCCRGTSTROGGTCRGLIFTSCSSTROSCRGGTCRGLIFTSCSSTROCCTCG$	430
Ebjet	351	TOTOCTCADDRETTACCAGOGGCCCCTTACCCAGTGCAGGCCCGCCCGCGCACCCCCC	7976
2mery	433	SCHTATOSTOTI FRACARGACGGAAGGGACGTOSDSGCTOCTSTGCTCCTCGCSCCTCTAA	490
Sbjor	1911	PCTORTGGTCTTTGACARCRCRARGERARGERAGGTGCTCTTTTTTTTTTTGACARCRCRARGERARGERAGGTGCTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1079
Ouery	491	OGCCAGGGTAGCCSGACTAGCTGCCAGGGAGAGAGGGGCTTTTTTTCAGGGCACGGAGCCACCTC	559
20,000	1071	OTORYOPERORDEDATORETTOROUGHORAGERORITOROUGHORAGOROUGHOUGH	1190
Odex7.	881	DGA-9/T9GA/COTGUGAA/CGG/CSPS/SP/CAAIP99CA/OSTCGGG/CTT/TTTTPF/F9GA/CGA	610
Shjet	1131	CGASCIGGASSIBISAADBOOGGOCOCCANIGGCASSIDBBOOTTOTTCTGTGGGASGA	7130
Mery	611	GGGGASS TSCCCACACCCAGAGGCTSCTSGASSTCATCTCCGTGTGAGATTSCCCAG	£70
9kjet	3193	GGGGAGGCTGCCCCCACACCCCAGAGGCTGCTGGAGGTCATCTCCGGTGTGTGATTGCCCCAG	1589
Query	671	AGGCCGTTTCTT09CC9CCATCTGCCAAGACTGTGGCCCAAGGAAGCTGCCCGTGGACCS	736
Sbjet	1281	ASSCCSIFICITSSCCACCATCTSCCAAGACTSTSSCCSCAAGAAACTSCCCGTSGACCS	7.270
Query	732	CATOSTOGGAGGCOGGGACACTAGCTTGGGCCGTGGCCGTGGCAAGTCAGCCTTGGCTA	795
Sbjet	1821	TRICGIGGGGGGGCCOGTRIATTRGGCTTGGCCGGTGGCCGTGGCAAGTTRGCCTTCGCTA	1370
2wery	793	TGATOSAPTACACCTCTGTGGGGGATCCCTPCTCTCGGGGGGCTGGGTGGTGACACTCGG	360
Skjet	1271	TOWN POWORD COLOREST CONTROL OF STREET CONTROL	1480
Cherk	653	CCACTGCTTCCDGRGCGGAACCGGGTCCTGTCCCGRTGDCGATGGTGTTGCCGGTGCCGT	BIG
Shjet	3631	CORCIGOIDODRAGOSORACOSOGICOTERIODERISSOCIAGTOTETECCOSERSCOSI	2480
Query	511	POCCASOCCTCTCCCCACCTCTCCACCTGCAGCTGCAGCTGTGTTTATCACCACGGGG	910
Sbjot	1491	GEOCCAGGCCTCTCCCCACOGTCTGCAGCTGGGGGGTGCAGGCTGTGGTGTACCACGGGGG	1559
Smerk	971	CTATCTTLCCTTTCD#NEXCCRACAGCGAGGAGAACANCAACAATATTGCCCTGGTCCA	2030
Shjet	1881	DIATOTTO COTTTUGGGACLCCAACAGOGGAGAGAGGACAGGATATTSCCCCT90TCCA	1615
Query	1931	CCCCCCRGCCCCCGCCCCCCAGAAAAACACACCCCAGCCCGCTTTTTCCCCCCCAGCCGCCGG	1099
Sbjet	3631	CUTCTTCRSTTCTCTGUCCTURCASATACATCCAGCCTGTGTGGCCTCCCAGCTGCTGG	2670
Query	3090	CCAPPOCTGGTGGGTAGGCAGATCTGTACCGTGACGGGGGGGGGG	1180
Sbjet	1527	COASSCUTSTOSATOPTAAGATCTSTAGGSTGAGGGGCY999PGGAAGAGSCAGTACTA	1786
Chery	3151	TWGCCAACAGGCGGGGTCACTACCACCAGGCGCCTCAAGTCCCCACAGTCCACCACCAGGACGCCTG	1230
S0jet	1731	TODOCRACAGOCCOGGGTACTOCAGGAGCCCCAGACCAGATCAGGGAATGAGGATOTOTO	1795
Cuery	1211	CATGGCCTGACTICTATPSRAAGCGARACCCCARGATSTTTTTGCCGGCTACCC	1279

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Series 1784 CAATGGCGCTGACITCTATGGAAGCCAGATCAAGCCGAAGATGTTCTGTGCTGCCTAGCC 1880
Query 1271 CGAGGGTGFFATTGATGUCTGUCAGGGGGACAGFTGTGTGTGTGTGTGTGTGTGAGGAFAG 1930
Sbjet 1881 0780007900ETIGNTSCOTOPTAO9009ECAGGGGTGGTCCCTTT7FFFFGGGGACEG 1910
Shjet 1911 CAPCICTOSACGCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCACTGGTGTGC 1970
Query 1891 COMMODOUNMARGUCAGGGGTGTACATCAAAGTGAGTGAGTTGCGGGGAGTGGATGTTGCR 1880
Fbjet 1971 CUTGGCCCAGAAGGTAGGGGTGCGCGCAAAGTCAGTGACTTCCQAAGTGTGCCACGGGTGTTCCA
Query 1481 SECRIARAGACTCACTCURAGGUAGGGGCATGGTGACCCAGGTGGGGGGGGGTGGGTTC 1510
Sejem 2031 9900ATRABAGACTCRCTCC98A900AGC99CATUGEGACCCAGCTCTGACG9GTGGCTU 2090
Seven 2341 GAPOGRAGATTITETTETPOPPONOGFCCACAGGTCCAAGGACACOOTOCCTCAGGG 2210
Query 1681 TOSTSTETTOCKCROTGGGGGGGCCACTERSDOCKGROCKCCCARGUTCACDCTOTTS 1680
Query 1681 ACCCCRESTRARIESTECTSCESTCESGREECCCESTERFST90000TGREGREGS 1750
Shipet 2271 ACCCCCARGINANTATTGTTCTGCTGTCTGGGACTGGTGTGTGTGTGCCCCTGATGARGG 2930
Query 1781 GATOCTUTTARATRATARAGATGGTTTTGATT 1783
Secon 1981 GATGOTOTTRAATRATAAGATGOTTTTGATT 2868
```

(444)

Store = 371 bits (168), Expect = 4e-59 Identities = 153/183 (1006), Gaps = 5/193 (08) Strand=Flus/Plus

Spran	0=513	2/2108	
Query	1	POSMOCCOCCTTCCAGGGACOCTAGCCTGAGGGCCCACAGGTGAGGCAGACCTGGCCTAGC	69
Sbjet	1	TOGASOTO POTTTO CROSSACCOTACCTGASS POOTRORSOTGASSCERSCOTESCOTE PO	80
Query	€1	APSYCCAGGCCACGCCCCCCCCCCCCCCCCCCCCCCCCCCCC	120
Shirt	62	AGRICUCTACGOTACTGCCTCTGCCTCCAGGCCGCCTGCTGCTGTGGGAGCCACCATGCTCT	120
Query	121	TGCCCASGCCT99AAACTGRCCCGACCCCSSCRCTACCTGGAGGCTCCGCCCCCACCT90	180
Sbjot	121	TGCCCAGGCCTGGAGACTGACCCGACCCCGGCCCTACCTCGAGGCTCCGCCCCCCACCTGC	180



Blast 2 Sequences results

Erénz BLAST DANS Esignativ Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2,2.14 (May-07-2006)

Marchi Manusch 2 gap open 5 gap extension 2

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C Show CD translation 400

Sequence 1. iciseq_1 Length = 1783 (i . 1783)

Sequence 2: gill2065ismb;N07002-1;H sapiens liver mRNA for serine protesse hepsin Length = 1199 (1...1199)



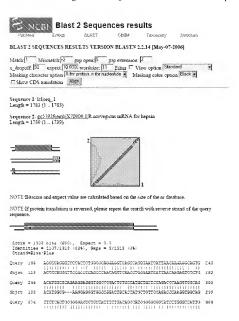


NOTE. Bitscore and expect value are calculated based on the size of the ar database.

NOTE If protein transission is reversed, please repeat the search with reverse strand of the query sequence

Score = 2208 bits (1199), Expect = 0.0 Identities = 1195/1199 (100%), Gaps = 0/1199 (0%) Strand#Flus/Flus

Shjat	121	GACCGCAGGAAGCTGCTCTTGTACCGCATCGTGGGAGGCCGGGGATACGAGCTTAGACCGG	190
Dwery	337	TGGCCGTGPCAAGFCAGCCTTCGCTATGATGGAGCACACTTTTFFF9999AATGCCTGCTC	829
Sbjet	181	TOOCOSTAGGAAGICAGCCTICOSTATMATORAGCACCCCCIGIGGGGGGAITTTTTTTTT	240
Shery	925	TCCGGGGGCCGGGCCGACAGCCGCACTGCTTCCCGGGGCGGAACCGGGGCCGGAACCGGGCCGGAACCGGGGCGGAACCGGGGCGGAACCGGGGCGGAACCGGGCGGAACCGGGGCGGAACCGGGCGGAACCGGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGAACCGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGAACCGGGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCAACCGAACCAACA	894
Stjet	241	IQUESTRONACTOROTGECTARCAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	300
Query	585	DSATUPONAGROTTTGGCGGTGCCGIRGGCTAGGCCTCCGGGGCCTGCAGCIRGGG	344
Bbjot	301	CONTROLOGYGICITTSCCOUTPOONTGGCCCAGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	365
Owery	948	SISCREDITSTOSPCIA/CACHGEGGITTCTTCCCTTTC99GRCCCCAACAGUGAGGAG	1964
Sbjat	361	GTGCAUGCTGTGTCTACCACGGGGGGCTTATCTTCCCTTTCGGGACCCCTAACAGCAGCAG	420
Onery	1005	AACAGUAACGATATIGOOODOPPOUROUTOTOCAGTUUCCTGCCCCTCAGAGATRAATO	1064
Shock	421	ANCAGCAACGATAIT9000TG990CRCCTCTCCRGTCCTCTG9000CTCACAGAATACATC	455
Query	1965	CASCCTOTOTOCCCACCTOCTOTTAGGSCCCTGGTGGATGGCAAGATCTTTACTGTG	1124
Boget	481	CAGCCTGTGTGCCTCCCAGCTGCCCGCCCCTGTGTGGCAAGATCTTTACCGTG	840
Query	1125	AGGGGTP999CARCLGCCAGTACTATGGGCAACAGGTP9999TACTCCAGGAGGCTCGA	2194
S ಕಟ್ಟೆ ಇಕ	541	acobicty) document constructions and account term and account to the construction of t	633
Dreza	2188	GTOCCCRIMATEAGTAATDATGTCTGCRATGGCGCTTGCTTCTATGGRAMCCAGATCRAG	1244
Mbjet	108	GTCCCCMTMATCAGCRATGRTFTCTGCRRTGGCGCTGACTTC2ATGGRARGCRGATGRAG	560
Query	1245	OCCRAINATESTUTESTECTRECTROCOCRAGGETGECHTURTECCTGCCCAGGGGTACAGC	1804
Sbact	661	OCCABURISTICIBITESCIROCOCCAGGGTGGCRIGRIGOCTSCCRASSVOSRCRGC	720
Query	1095	SSTSTTCCTTTSTSTSTSAGURCASCATCTCTCDSRCSCCACCTTSSCCUSCTSTSISSC	2364
805 ಬರ	721	POTENTO DUTTTO TOTOTO TO ANGLA CASCATCICIO PARO AD LA CONTROLO DE	780
Query	13-65	ATTGTUAGTTUGGGCACTGGCCGTGGCCCGGGCGGGCGGCGTCTACACTGAAGTC	1424
30300	791	ATTGTGAGTT9999CACTGGCTGTGCUCTGGCCCAGAA9CCAG9GGTCTACACCAAAGTC	545
Quexy	1428	AGTGACTTOUXXAGTGGATCTTCCAGGCCATAAAGACTCAGTCCGGAGCCAGCC	1454
Hoget	941	AGTGACTTCCGGGAGTGGATTTPOCAGGCCATAAAGACTCACTDDGAAGCCAAGCGAGCAC	900
Sperk	1488	GTGACCCASCTCTGACCSGTGGCTTCTCGCTGCSCAGCTTCTAGGGCCCGAAGTGATCCC	15+4
§ ಶಿಕ್ಷ ಚಿಕ್ಕ	951	GTGACUCAGCTCTAACCGGTGGCTTCTCTCTCTGCAGCCCCCAGGGCCCGAGGTTAATCCC	365
Query	2545	OGIGGIGGAGCACGCTGGGCCCAGGATGGGCCGTTTTCTTCTTGGGCCCCGTCCACA	1604
9hjet	961	GGTSGT099ATVCACGCTGGGGGGGGAGGATGTGTTTTTTTTTTTGGGGGGGG	1029
Query	1608	STOCKLYSKOROCOTOCOTOCKSSTOTTCTCTTOCKCKGTGAGGGGCCCACTCRSDTC	1664



fbgit	240	$\tt otcoccoscoscoscoscoscoscoscoscoscoscoscosc$	299
Duezy	364	TOGOTOTTCTCLTCASCASTORCTAGOLOGCOCTGTACCCAGGTGCAGGTTAGCTGTGGGG	423
Skjet	200	PRACTATECTACTACTACGGAGGGACCAGGAGCCACTGTACCAAGTGCAGGTCAGTCCCGGGG	353
Query	424	ACSCROSQUEGREGGECTTEGGCGGGAGGGGABDSEBCSEGGGGGGGGGGGGGCGCTGTC	433
Thick	360	acictopacifitestst teghuragaurgroggracgtsgresctstestsutottcac	419
Stern.	484	GCTCCLACSCTAGGGTAGCIGGACTCAGGTGCGGAGATGGGCTCCTCAGGGCALTGA	543
Sbytt	420	GCTCCAACGCLAGGTAGCAGGGCTCGGCCGAGGAGAGATGGGCCTTTCTCAGGGGTCTGG	679
Sterk	564	CCCACTCCGAGCTGGACTGCAACGGGGGGGGGGGGACTGCACGTCGGGCTTTTTTCTGTG	603
೮೮೨೦೮	489	DENNITURARIO CONTO	525
Query	604	PROGRAMMAGALTECCOCATACTCAMAGETISCHUGRGUTCATCTCCGFGFGFGAIT	663
Shint	840	TOTACUAGGCCGGTCTSCCTCTSSCTCAGCCGGTTGCTGGATGTCATCTCTGTATSCCAACT	599
SWEEN	564	SCHOOL BASSOCCOTTOTICGCCGCCATTSCCAAGACTGT990CCCGGGAAGCTGCCG	>23
86505	600	FTUCTAGAGGCOGATTCCTGACTGCCACTGCCAAGAGCTGTGGGGGGCAGGAAGCTGCCGG	655
Oner?	724	TGGACCGCATCGTGGGASCCOSSACACCAGCTTGGGCCGGTGGCCGTGGCAATCAGCC	783
Sbjet	860	TOGRITOSCATIFIPOSOSOCCAGUACAGCCCTOSCAAGATSSOCATOSCAGUICAGCC	729
Query	784	TTCGCTATGATGGAGCRCRCTTTTTTTGGGGGTCCCTCCTCCCGGGGGCTGGTTGTTGA	348
Shjat	720	TOCGTTATGATGSGSACDCACCTCTGTGGGGGATCCCTGCTGTCCGGGGGACTGDGTACTGA	779
Query	244	PAGE OPEN ACT OF COMMAND SERVICES OF THE CONTROL OF T	503
కల్పడ	786	DOSUTSURURUT GUTTTOURGRERARIDESETTUTGUTGTUTGGGTGGOSRGERTTESETS	733
Donny	904	STSCCGTGGCYTASSCCTCTCCCCACGGTCTGCAGCTGGGGGGTGGAGGCTGTGGTCTACC	963
\$63cc	940	STSCTSTA9000000ACCTCACCTCATGCCGTGCAGCT99999STICAGGCTGTGATCTAIC	253
Query	H64	ACCESSOR TO THE CONTROL OF THE CONTR	1923
Ebjet	900	ATGUNGLIACITETETTTTTAAGAGOTACTATGUNGAAAACAGETATTTTTTTTTTTTTTTTTTTTTTTTTTTTT	959
Speni	1024	IGGICCACTTTTCGAGCCCCTGCCCCTCCACAGAATACATCTAGCCTGTGTGCCTCCCAJ	1083
20222	560	PROTOCACCTUTCTAGUTOCUTTCTTCTTCACAGAATACATCCAGCCGGTTTGTCTCTCTG	1019
Query	7085	CTGCCUGCCAGGCCCT9GT93AT99CAAGGTGTGACGGTGACGGGCT9G99GAGAGAGCC	1148
ಕರ್ಶಾ	3020	STEDEPERCASOCOCTOUTUGACGGLAAGGTCTGTACASTCACCCGCCTGUGUTAACALAC	2075
	1144	ASTRUTATIOGCULACASSCUSSISSIACTTUCASSASSCUSCOCATARICASCASCAATS	1203
Shjet	1080	agtectrosgorageragetgtggtgctccragaggcccgggtcccratragcarcg	1139
Smarl.	3204	ATSTOTECHAP90000T9ACTTCTATGGRAROCAGATCHAOOTCARGATGTCTGTGCTG	3263

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Sbjet 114) ARSTYFROMAUROCOCCORCTTCTROGGGAATTAGAFCARACCCARGATGTTCTGTGCTG 1155
Query 1004 OCERCOCCERSOSISSISTICATESCIPOCERSOSCERARSOSSISSISSICCITTIGISISIS 1000
Street 1980 AGGACAGAACCTCTGGAACATCAAGATGGCGGCTCTGCGGCATTGTBAGCTGGGGTACGG 1818
Query 1884 GUTGTGCCC1GGCCTAGAAGCCAGGGGTCTAGACCGAAAGTCAGTGACTITCCGGAAGTGGA 1848
Sejet 1820 GERFATTTGGCCCGGAAGCCGGGAGTGACACTAAASTCATTGACTTCCGGGAGTGGA 1175
Query 1444 PYTFOCKGGCCKTKKKGGCTCKCTOTOKAGOTAGOGGCKTGGTGKCCCKGCTCTGKTC 1501
Stret 1883 TOTTOCKOCCATAAAGACTCACTCCGRAGCTRCCGGCATGGTAACTCAGCCCTGACC 1487
                  1.1.1
 Score = 77.6 hats (40), Expect = 1s-10
Identities = 175/230 (765), Gaps = 8/230 (34)
  Strand=Plus/Plus
QUERY 1888 ICCACROTOPOCCGARGATGUGACGITTITCTTCTTGGPTCCGCACGGCCCGAAGGA 1614
Selet 1817 TOTACACTYPOPOCTCACATGRACGCTTTTTTPCTCPATCCAGTCCATAGRATCCAAGGA 1876
Query 1816 CACCOTCCCTCCAGGGTCTTTTTTCCAGGTGGCGGGGCCCACTCAGCTCCGGAAACCACC 1874
Shjer 1877 IGC-- TOGGTOTAAGGACTICICITCURCAGTGGCUGGCUCACTCAATUCCAGUGCUATI 1834
Quary 1878 CARCIPIADOCPOCTORCOCCCRYGIARATATIGFTCPDDISTCF000GA-CTCUTGTCTA 1733
Sbict 1835 09-COTCACCUTIONA-DESCRIPTIONALITY TRANSPORTED TO THE STATE OF THE STATE 
Owers 1734 GUIGOCOCCIGRICATGGGATGCTCTTTRARTARTRAGGTGGTTTTGATT 1783
Sbjet 1692 SECONOCCITOTOC--GGRISCICITIAAATAATAAAAGUIGGTTTTGATE 1789
 Scare = 68.1 bits (04), Expect = 6e-07
Identities = 68/85 (67%), Gaps = 0/88 (0%)
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 Query
 89
 SSCREENDANTECTGATGGGGGGCCAGGATGCTCTTSDDCAGGGGCTGAAAACTGACCC
 148

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